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OIKE

RAW SEQUENCE LISTING

DATE: 11/27/2001

PATENT APPLICATION: US/09/825,293

TIME: 14:04:25

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Output Set: N:\CRF3\11212001\I825293.raw

ENTERED

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3 <110> APPLICANT: FARWICK, MIKE
4     HUTHMACHER, KLAUS
5     PFEFFERLE, WALTER
7 <120> TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES WHICH CODE FOR THE MIKE17 GENE
9 <130> FILE REFERENCE: 21123/280108/MAS
11 <140> CURRENT APPLICATION NUMBER: 09/825,293
12 <141> CURRENT FILING DATE: 2001-04-04
14 <150> PRIOR APPLICATION NUMBER: DE 100 47 867.0
15 <151> PRIOR FILING DATE: 2000-09-27
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: PatentIn Ver. 2.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1890
23 <212> TYPE: DNA
24 <213> ORGANISM: Corynebacterium glutamicum
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (252)..(1673)
29 <223> OTHER INFORMATION: mike17-Gen
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34 ctttgcgcag gtgacacaat tatcccaaca gttgcaccgt aggtgcctaa aaagttcccg 120
36 gggcggatgt ggcccgacca cgccgggcac ctggtggcgg cgggctgcgt cgaaaagcga 180
38 aaatcaacaa gtttgcaaca cctcagtgcc aagagtgggt aaggtgatgg tgatcacgct 240
40 atagttgcgc c atg gga aag aca tat gtg ggg tcc agg ctg cgc caa ctg 290
41           Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu
42           1               5               10
44 cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338
45 Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly
46     15               20               25
48 tta tct gca agt tat gta aat cag att gag cac gac gta cgc ccg ctc 386
49 Leu Ser Ala Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu
50 30               35               40               45
52 acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca 434
53 Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala
54           50               55               60
56 acg ttt ttc tcc cgc gac gat gac tcc cgc ctg ctc gcc gag gtc caa 482
57 Thr Phe Phe Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln
58           65               70               75
60 gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa 530
61 Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln
62           80               85               90
64 gag ctt tcg gag atg gtg tac aac cac ccc caa cta gcg cgc gcg atg 578
65 Glu Leu Ser Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met
66           95               100              105
68 gtg gaa atg cac cag cgt tac cga aac gtg cgc gat aag ttc tcc atc 626
69 Val Glu Met His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile

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70	110		115		120		125	
72	gca	gtg	gat	aat	cgc	acc	aac	acg
73	Ala	Val	Asp	Asn	Arg	Thr	Asn	Thr
74								
76	gag	gcc	gtg	agc	atg	ccg	cac	gaa
77	Glu	Ala	Val	Ser	Met	Pro	His	Glu
78								
80	cgc	caa	aac	tac	ttc	gat	gcc	ctt
81	Arg	Gln	Asn	Tyr	Phe	Asp	Ala	Leu
82								
84	gcg	caa	ctg	ggc	tgg	cag	ccg	tac
85	Ala	Gln	Leu	Gly	Trp	Gln	Pro	Tyr
86								
88	atc	gcc	cgc	cgc	ctg	caa	atg	gat
89	Ile	Ala	Arg	Arg	Leu	Gln	Met	Asp
90	190							
92	aaa	gag	gaa	tcc	ggc	acg	ctg	cac
93	Lys	Glu	Glu	Ser	Gly	Thr	Leu	His
94								
96	ctg	aca	atc	cac	gca	cgc	ctc	aac
97	Leu	Thr	Ile	His	Ala	Arg	Leu	Asn
98								
100	gcc	acc	gaa	ctc	ggc	tac	cta	gaa
101	Ala	Thr	Glu	Leu	Gly	Tyr	Leu	Glu
102								
104	gtt	gac	gac	ggc	atc	tgg	tcc	acc
105	Val	Asp	Asp	Gly	Ile	Trp	Ser	Thr
106								
108	cgc	ggt	gtg	gcc	tcc	tac	ttc	gcc
109	Arg	Gly	Val	Ala	Ser	Tyr	Phe	Ala
110	270							
112	atc	ttc	cac	tcc	gag	gcc	gaa	aaa
113	Ile	Phe	His	Ser	Glu	Ala	Glu	Lys
114								
116	ggc	caa	ctc	ttt	ggc	gtg	ggc	tat
117	Gly	Gln	Leu	Phe	Gly	Val	Gly	Tyr
118								
120	acc	ctg	cag	cgc	ccc	aac	ctg	cgc
121	Thr	Leu	Gln	Arg	Pro	Asn	Leu	Arg
122								
124	gtc	gac	cgc	gcc	ggc	aac	atg	tcc
125	Val	Asp	Arg	Ala	Gly	Asn	Met	Ser
126								
128	cac	ttc	acc	cac	tac	ggc	ggc	acc
129	His	Phe	Thr	His	Tyr	Gly	Gly	Thr
130	350							
132	acc	ttc	acc	aac	ccc	ggc	caa	gtg
133	Thr	Phe	Thr	Asn	Pro	Gly	Gln	Val
134								

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136 gac gga cgc aac tac ctg tgg atc tca cgc acc gtg cga cac cac gaa 1442
137 Asp Gly Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu
138          385          390          395
140 gcc cgg ttc ggc gaa gta gac aaa atg ttc gcc atc ggc ctg ggc tgc 1490
141 Ala Arg Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys
142          400          405          410
144 gaa gcg cgc cac gcc gac cgc act gtg tac tcc cgc ggt ttc aac ctc 1538
145 Glu Ala Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu
146          415          420          425
148 cag gac ctc tcc acc gcc acc ccc atc ggg tcc ggc tgc cga gtg tgc 1586
149 Gln Asp Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys
150 430          435          440          445
152 acc cgc gag aac tgc gcg cag cgc gca ttc cca tcc gtc cac ggc cgc 1634
153 Thr Arg Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg
154          450          455          460
156 atc aac atc gac gcg cac gaa tcc act atc gcg ccg tac taagaaaagg 1683
157 Ile Asn Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
158          465          470
160 agcttgcttt acgacgcacc ctgcgggggt gggttttacc ttttatgaat gatcagcaat 1743
162 atccgcgtaa acaccatcgg tagccagaag aacatcatcc ggggcgataa tcagggacca 1803
164 cccgcgtcgc cctgcgtga cgtagattcg ctcttgaga attgcagact catccaaaaa 1863
166 cagcggtgc ttgttcttct gccctat 1890
169 <210> SEQ ID NO: 2
170 <211> LENGTH: 474
171 <212> TYPE: PRT
172 <213> ORGANISM: Corynebacterium glutamicum
174 <400> SEQUENCE: 2
175 Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu Arg Arg Glu
176 1          5          10          15
178 Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly Leu Ser Ala
179          20          25          30
181 Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu Thr Val Pro
182          35          40          45
184 Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala Thr Phe Phe
185          50          55          60
187 Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln Asp Val Met
188 65          70          75          80
190 Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln Glu Leu Ser
191          85          90          95
193 Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met Val Glu Met
194          100          105          110
196 His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile Ala Val Asp
197          115          120          125
199 Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala Glu Ala Val
200          130          135          140
202 Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala Arg Gln Asn
203 145          150          155          160
205 Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala Ala Gln Leu
206          165          170          175

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208 Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser Ile Ala Arg
209           180           185           190
211 Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser Lys Glu Glu
212           195           200           205
214 Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu Leu Thr Ile
215           210           215           220
217 His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met Ala Thr Glu
218 225           230           235           240
220 Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile Val Asp Asp
221           245           250           255
223 Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile Arg Gly Val
224           260           265           270
226 Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys Ile Phe His
227           275           280           285
229 Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu Gly Gln Leu
230           290           295           300
232 Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser Thr Leu Gln
233 305           310           315           320
235 Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg Val Asp Arg
236           325           330           335
238 Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe Thr
239           340           345           350
241 His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe Thr
242           355           360           365
244 Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly Arg
245           370           375           380
247 Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg Phe
248 385           390           395           400
250 Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg
251           405           410           415
253 His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu
254           420           425           430
256 Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg Glu
257           435           440           445
259 Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg Ile Asn Ile
260           450           455           460
262 Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
263 465           470
266 <210> SEQ ID NO: 3
267 <211> LENGTH: 19
268 <212> TYPE: DNA
269 <213> ORGANISM: Corynebacterium glutamicum
271 <220> FEATURE:
272 <223> OTHER INFORMATION: Primer mike17-int1
274 <400> SEQUENCE: 3
275 aatggatcac gatgtcacc
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 19
280 <212> TYPE: DNA

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281 <213> ORGANISM: Corynebacterium glutamicum

283 <220> FEATURE:

284 <223> OTHER INFORMATION: Primer mikel7-int2

286 <400> SEQUENCE: 4

287 tagtgggtga agtggaagc

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VERIFICATION SUMMARY

DATE: 11/27/2001

PATENT APPLICATION: US/09/825,293

TIME: 14:04:26

Input Set : A:\280108ma.app

Output Set: N:\CRF3\11212001\I825293.raw